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009290" 24050960

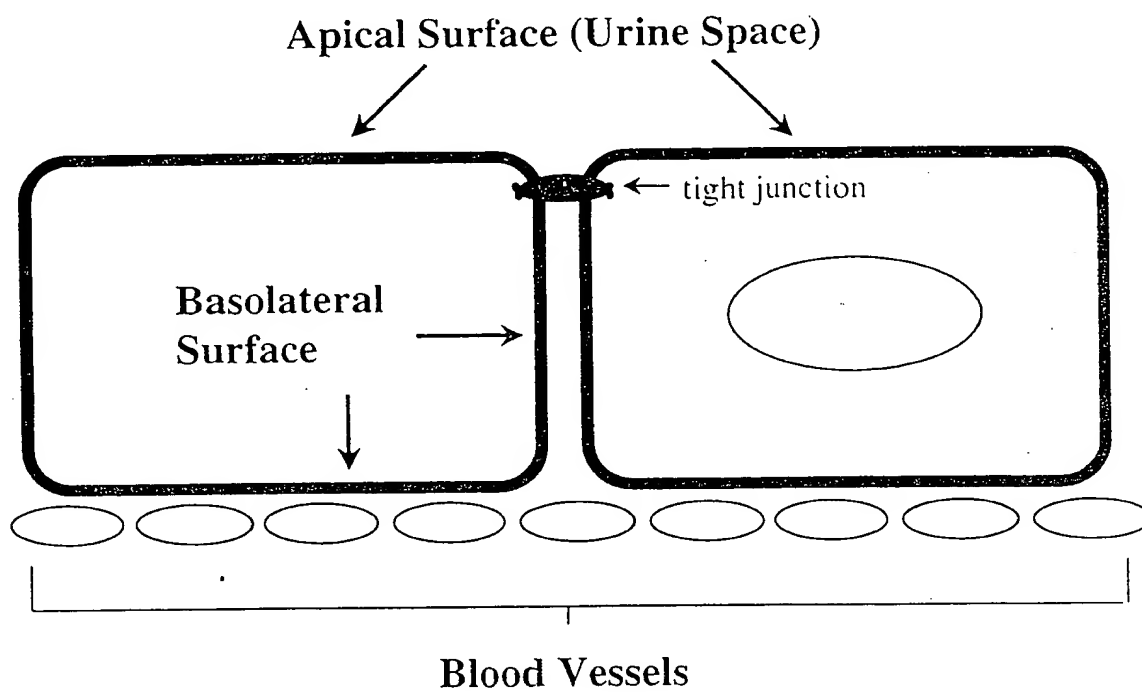


FIG. 1

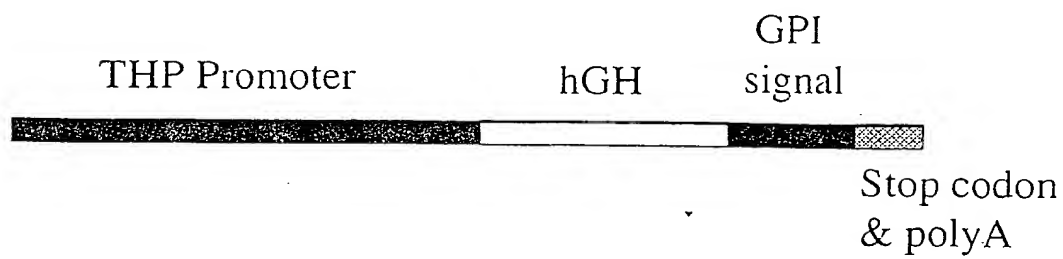


FIG. 2

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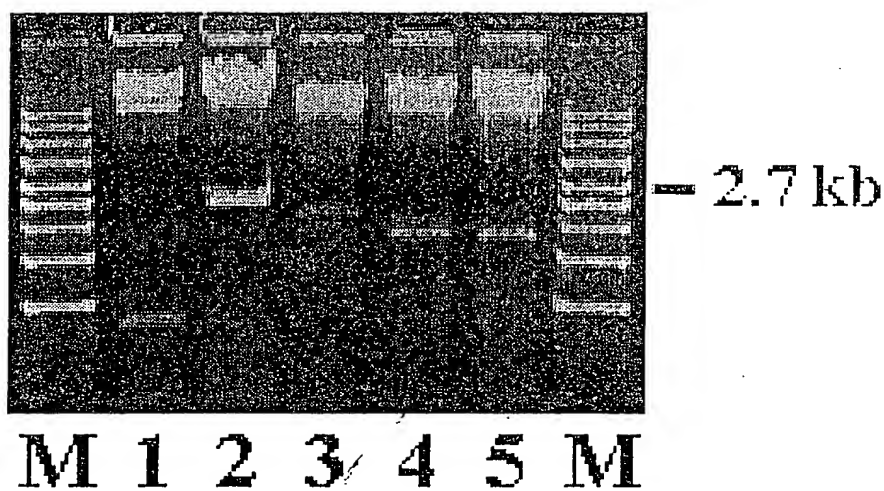


FIG. 4

Probes

5'-

- 2.7 kb

Mid-

- 2.7 kb

3'-

- 2.7 kb

M 1 2 3 4 5 M

FIG. 5

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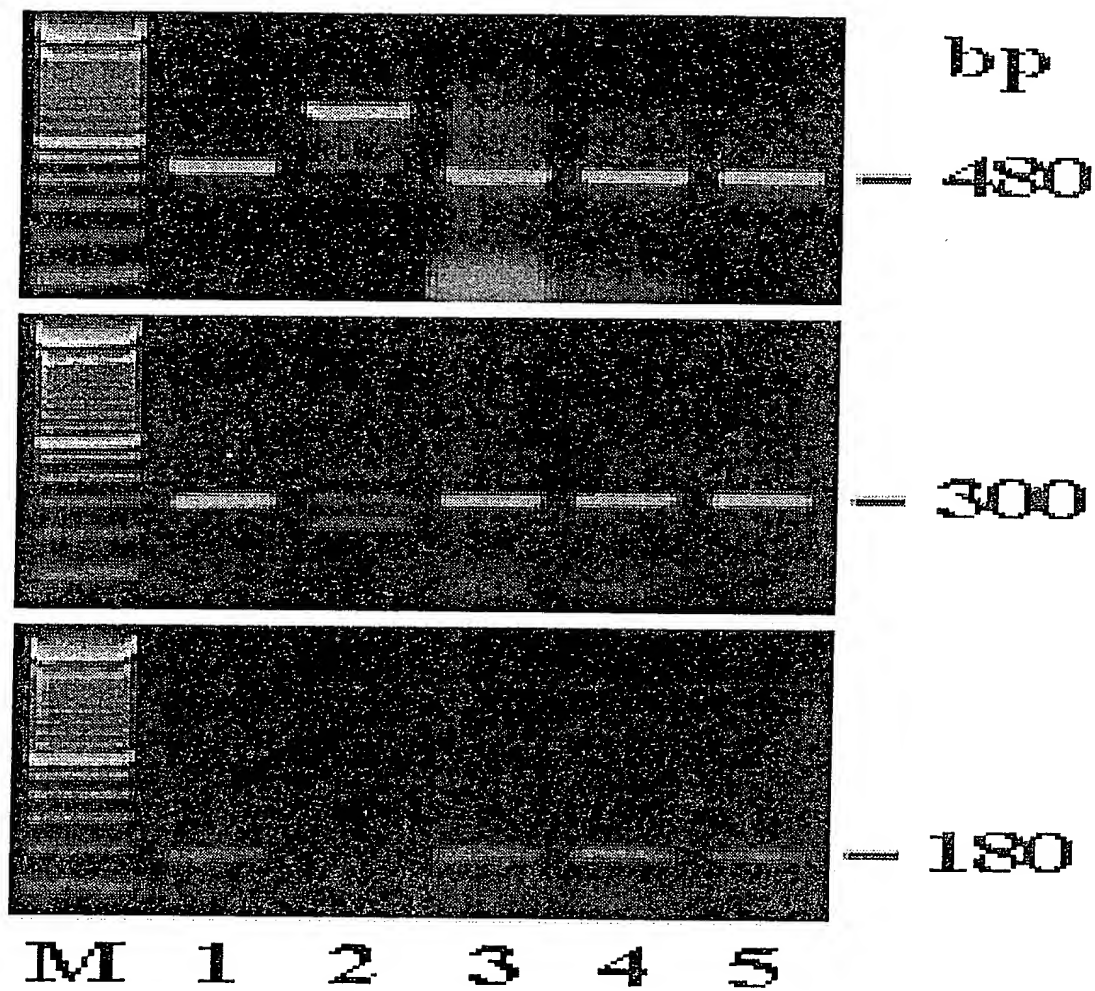


FIG. 6

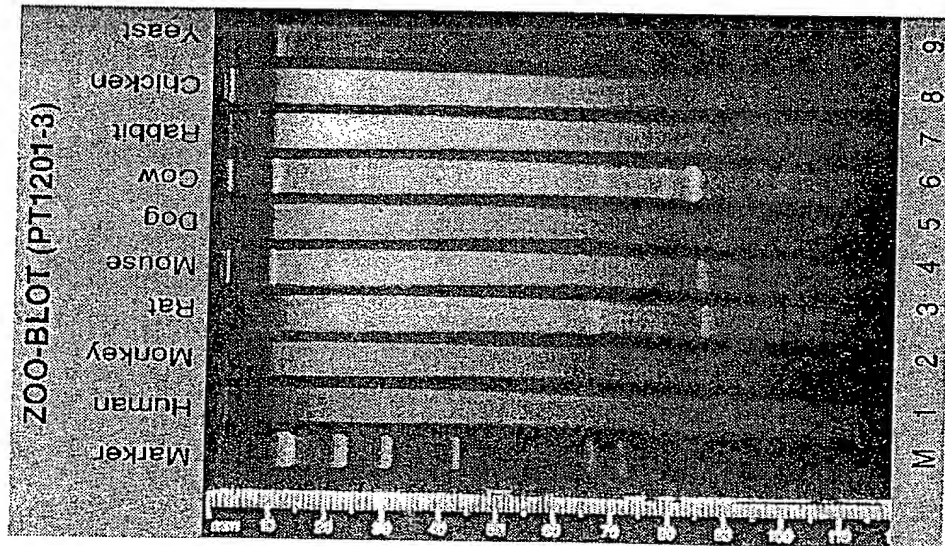


FIG. 7A

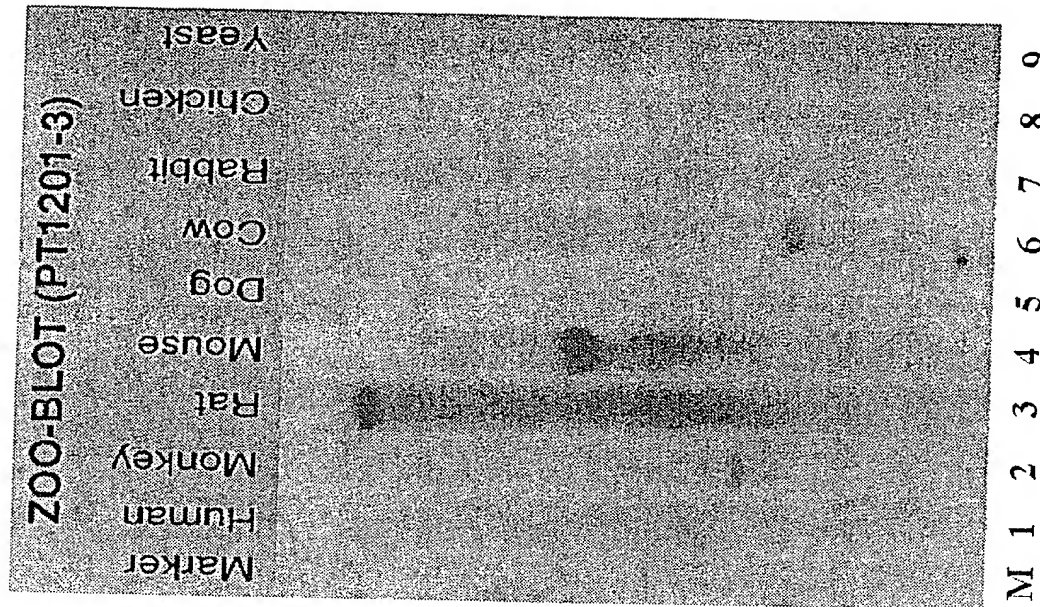


FIG. 7B

THP Gene Structure

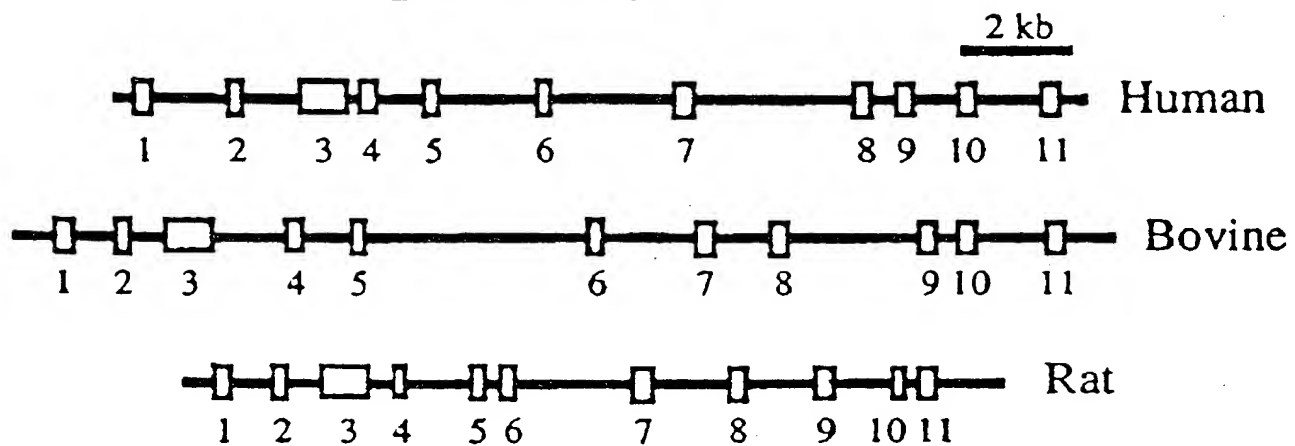


FIG. 8

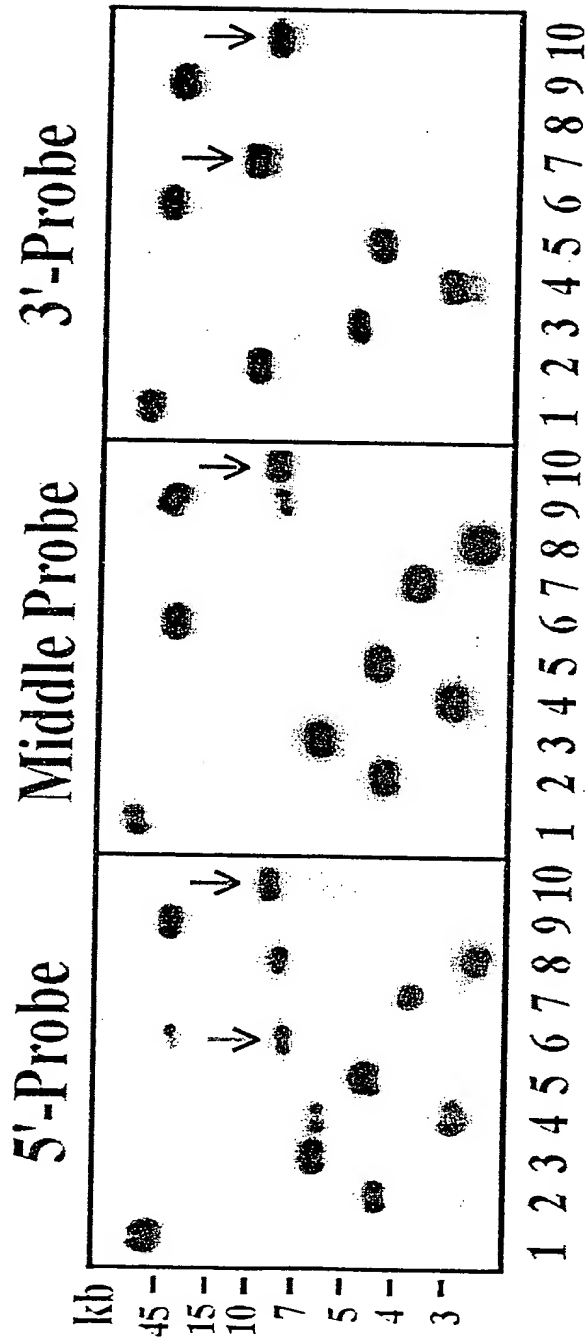


FIG. 9

1 GGGG/GGGCCC TCGGGAGTTT GGCTAAGTCT TGCAAATGAG CTGTGATGAC
polycloning site of pBS
 51 AGGTTTGC GC CATATGAGAT CCAGTGACAA GTCATCTCT AGATGTCTGC
 101 ATACCAATAA GTGACCCATC ATTATGCAAT CAGGCCGGAC TCATCCTCTG
 151 TGGCTTTGTC TCTTACTACT GTAAACTTGA TAACCTATAT GATTTTACCC
 201 ATTTCCCCTC CATGGCACTC AACTCTCCTC TTCCTATGTG ACCCTACTTA
 251 TGTCCTATGT GACTCCAGCT GCTTCCTTTG ATGAGAGCCA TCCTGTTCTT
JP.S3
 301 TCTATGTGAC TCTGCTCACT TCTTCCACGT GACTCCACCA ATCTGTCTAC
 351 ATTGCAGAGT CACTCACAGT TTCTTGAGAG CAGAAGACTC AGAACTGATC
 401 TGTCTCAAT GTCCTCCCTA CACTTTCTCC TCATAATCCA CATATCTAAA
 451 GCTATAGAGA TAATTTTCATG CACTATAGCT TTCAGTACTA TCGTATCTAC
 501 TGTCTCTACC CTGTAAGTGG TATCTTCATG ACATCTCGAA TATTTCCAAT
 551 TTCTCTATTG CTGCAAAGTC TTGAGAAGTC TAGTCTTATG GATCTCCTTT
 601 TCTCCTCAGG TCTCCTGGTC TCCACACACC ATTCACACTT CTTGAATATT
JP.S4
 651 CTTTGAACAT AACAAATTCT CTCCATGGGT TTGTTCCCTC TACCCAAATT
 701 CATGCCTTCA GGATACTTAC TCTGCCCCAT CTTCACTCAT CTCTGCTTTG
 751 GTCATTCAAA TCTCAAATGT AGCCATTTCT AAAAGGCTCT CCAAGAGAAT
 801 AATATTTGAA AGCATTTTGC TATTCTATCA AGTGATCATA CAATGTCTGC
 851 TCCTGCCACC ACCATGACCA TCCCCATGAA TACAGACACT GCCTTCTTAG
JP.S5
 901 TGTTTGCTGT ATGTGTTCTG TGTGGTACAT TGTAAGATAA TGCTGTAATA
 951 AACATCTGTG GAGCAAATTG AATCATCAGA TAGCACCCCTC TCTCTGAGAG
 1001 GCATGATCTC ATGGTTATCC CCAAAGCATG AGGTAAGGAC ATTATCCCAG
 1051 GTCCATGCTG GTTCCGTAT TGATTGTTTC TAACACAAAC TTAATAGATT
 1101 AAAACAGCAC GGATTTATTC TCACATGTTT TGAGACGCCA GAAATCTGAC

FIG. 10A

1151 ACCAGTTTCA ATGTTTAGAC TTGATGCACA CCTGTAATTC TGGTACTTAG
 1201 GAGGCAGATG CAGGGGGACT ATGATTTAAA GCCCATTTTT AAGCTGCTGG
 1251 GTGAGAACCT GTCTTGATTT TTTTTCACA TTGGGCTAAA AGTCAAGGAT
 1301 CATCAGGGTT GGTGCATTCT GGAAGAAACC TTTGCCTTGC AGCTTCCCAG
 1351 AGGGCCGCCA GCATTCCCTG GCTTGTGTTT GGTCTGGAA TCACTGTGAC
 1401 CTTATGCTCC ATCCTCACAT TCCCTCTGCA TTTATCCTCT AAGCACCGGT
 1451 GTGCTTGAT CCAACCTTTA GGAGCCCCAT AGATCCCCCA TTTCTCCTCG **JP. S6**
 1501 ACTTAATCAC ACCTGTATAA GTACTTTTCA CTCTGCAAAG CAATATTTGT
 1551 GGGTCCAAGG GATTAGGATG TGGGTATATT TGTGGGGTGT CATTATTCAA
 1601 TGCTTCATAT TTACACTGTT TCTCTGTTTC ACTTTATTGG GGTACTTGAA
 1651 CTTCTAAGAA GAACTGAGGG GTATTGTTGT AGGAACTAAA TTCCCCCATG
 1701 GACCTCTGTG CTTTCCACCT ATCACACAAG ACAGAGGGTA TTTGTATTTT
 1751 TAGATCCCCA GAAGAAATTC CCACTCTCAA CCCTCCATCC CTGACTTGCT
 1801 CACATCTAGA TGAAGCAGGG AACAGCCTGA GNCCTGGAAC TCACTGGAGC
 1851 CAGATGACTC TATGGAGTTA GGTTTTAGTA TTCAAGACAC GATGCAAGAC
 1901 TCACCTGCCT TCCCCTCACA GACATGTGGC TGCCTGTCAA AGGTGGGGCC
 1951 ATGGGGCTGC TGAGACTAAG TCACGTGGAC AGCGCCCATG ACAAGCAGTG
 2001 ACATGGAGAC CAAGGCTGCA GTGTGCATGC TCCACAGGTG CACCTGAAGC **JP. S7**
 2051 CTCAGAGACG GGAAGAGGAG AGGGAGCAGA AAGATGGGGT ACAGATACCC
 2101 CTCTGTTAGG AAGGGCTTCA AAACCGTCTT CTAAGTTTTT GATCCTTTTA
 2151 AATGTATCCA CCTGTCACTT GACCTCTCC TGCTCTGTCT GATCAGCTTC
 2201 TCAAAACCCT TCATCCCCTT AACTCCACCC TACTGAAAAA AGATGAAACC
 2251 ACTTGTCAAT ATAAACCTCA ACAGCTAAGC ATGGAATACT GTTAACCCCT
 2301 CAAGACATAA AGCTGACTGA AGGGATAAGT TTGAAAAAAA TGGGCTTCAG
 2351 TTTGCACTAG CTAAGTATGT AACCTTGAAG ATATTACTCA GTTTCTCTGA
 2401 ACTTCAGTCT GCTCTCCTAT TTATTGACAA CATGTAAGAG CACATACCGG
 2451 GCATTTCTTG TCACCAAATG AAGTTTCCAG TACCAGGAAT GGGTTATATC

FIG. 10B

3851 TCAGGGAGAA CCATAATCAG GGGGAGCCAT AATCAGGGGG AGCCATAATC
 3901 CAAGGGAACC ATAATCAGAA TATACTGTAT GAAAAAAATT CTATTTTCAA
 3951 TAAAAAAGA ATAAAAAAA AACAGTCTGA CTGAAGAATA GCACTTGGTA
 4001 AGTAACTCTT GTTATAACAA TCCATATCAA ATGCCCTGCC TGTGTTAGCA
 4051 AGTTAAGAGA AAAGATTATT CCAAGAGATC CAAGTCTCCT TCAAAACCAA
 4101 GTGTGTACAG AACATTGTCT GAGGAGTAAG ATTGCATTTG GCAACATGCA
 4151 TGTCTTTAAT GGTGTGGAGA ATTTCAGTGG AGTTGGCACG TCAGAAAGCA
 4201 CACTGGTGAA AAATGGAGAG AATAGATATA TCCTTTGAGA AATTTGGTCT
 4251 CAAAAGTAG GGTATCAAAT TACTTGGTGT CTGTGAGATC AATTGGTTGT
 4301 CTCTGTAGGT TAGCTTACAT AGGAGACAGG AATAAGTGAA GGAGAGAAGG
 4351 GAGGACATTG GAGCACCCAA GGAGAGAGGG ACCTTCCTCC TAAAAGTGAA
 4401 TGAGGTGGCC TTCATTCCAA GGAGAAGAGA TTCAGGTGCG CCGGGAAGAT
 4451 GAGGGACCAA CATCCACAAG GAATGGCAGG AAGTCATCCT GTGTGCATAA
 4501 ATGGAGAGAG GGGGTCAAAG ATGGAGCAAA GAAGGATGAG CAAGAAAATG
 4551 GTGGATGTGG ATACTCTGAG GATGGCCTGG CTGTGGTGAG CAAAATGTGG
 4601 GCAAAGTGGC ACTCCATGAA CAAGACAGCT TGCTCTGTTT GCAGATCCTT
 4651 AAATAAAGGC ACATGGCATG CCATGGAGGC TAGGGGAGTG GAGGGGAAAG
 4701 GTATATAGAT AGATGCAGAA GTACCAGAGG AGCCAGGAAG GACAGGAGTA
 4751 GGAGGGACAG GTTTGCACAA GGCTTTGTCC TCTCCCCACC AGCTCTCTCT
 4801 CCCTTCTGTA TATGCACATA CACAGTGAGC TAGTGTGCAT ATGTGTGCAC
 4851 ATATGCATGT GATGAACAGA GGCCAGTCTT GGGTGTGAGT CTTCAGGCCC
 4901 TATCTACCTT GTTTTTGAGA CAATCTCACT TGAGTGAGTT GAGTGACTCT
 4951 CCTAGTATTC TACAGAGGTT TCCTCAGGTG GGGAGGAATG GGTGGGAGAA
 5001 GCAAATTTAA GACTGGTTGA TTTCTTGAAT TTCAGTGGGC TTGGGAAATA
 5051 GCAGCTATAT ATTCAGTTTC CTCGTTCTTG GCTGGCTTCC TGGGGTGATC
 5101 AGAGCAGAGT ATAGTAGCCC TGTGTGGCAG TCACACCAAG CAGACAGAAG
 5151 ATAGGGCATG GCTCTGGTGT GGCTGGTAGA CATAGGAAAG GATCCTTGTA

FIG. 10D

6551 GGAGTGTCCA GATGGTCTGA TAACCTGATG CCATTCTCAG AGACTCTTTC
6601 CTGTCTGGAA TCTAGTGAGG AGGACTTATC TGGTGAAGCT GTCCTTTAGA
6651 ACAGGAGTGT GTTCCAGTCT TCAAAGCAAA CATTCCTTTT ATCCTAACAC
6701 AGTCTGACTT CAGATATACT GTCTTTTTTCC TGGCTCCTTG GGCTTAGGTC
6751 TACCTTGTCC TTGCCCAGGT CCAAGAAAAG GCCCAGAACC TTGGCACTGT
6801 TTTGCCAGTT AATGTCTAAC TGAGGAATGT CTTGCTGCCA AAAGGTGAAA
6851 ACAGAGACCT TGTATTTCCA GGCACAGGTG TGACCCCAAT GTCAATCATT
6901 TTGTGTCTAA CTCCCAGGGG AAAAATAAC AACAACAGAC TCATGGCTTG
6951 GAAAAGGTGA ATTCTATGCC AAAAGGGAAG GAAAGTTCTA CCCCCACAGA
7001 AACAATCTCA GAGGGCAGAA GCAGAGAATA ATCTGAGGGA GAGGGCCAGC
7051 CAAGGGCAGG CAAGTATATA TTGATCACAG GCACTTACTT GTGAATGGAC
7101 **CAGTCCTGTC** **CTGGGTTTCAG** **GTAAGGCTGT** **ATGAAACTGT** CACCCCCATA
7151 TCCACTTCTC CTCTATCTAA TCCCATTATA TTTCAGGGAG GTTGTGGTAG
7201 AAGCTTAGCT TCTGGACACT GGGGTCCCAT GCTAACCTTC ATGGCATCCT
7251 GGTATGCTGC TGTA AACCT AGGGTAATGC TTGCATCCAT CTGGAATTAT
7301 TTCACCTGTT GCAACCACAA TCATTTTGAA AATACTAGTA TGTATTATAG
7351 TTATGTATGT ATATAGAGTT AATCATCTCT AAAGCTCCTT ATCTTTTGCC
7401 ATTTCTTTAC ATGAGTTGTA TGAAGATGTA GACGATATTC ATTATTCTCT
7451 TTGGTATCTA GCACCTTGTT TGGCACATAA TACTACTCAA TAAGGGTTTG
7501 TTGAATGAAT AAGTAGGTGA GAGCAAATTG TAAGTTCAGG TAATCACGAA
7551 CTTCTGTGTA AACTCCAAGG CTGCCTCCAG TAAGGTATAA GTCCTGAGTG
7601 AGCCTTTCCC CATCTTGCAA CTTTTTGCTC CAAATGAAAG ACTCAGTTCT
7651 TCAAAATGTG CAGCACATGG AGGTTTGCGA CATAGGGGTG TATTCACAGA
7701 GGCTTCGGAA GCCCACCAAA CCTACAGTTA GATCACTGTA CAGTCTTCCT
7751 TTTACATACA AGCTGTGCCT CCTGGTNTAC ATCCATGCTG TTTTCTGATC
7801 CATATAGAGG GTACACAACA AAAGCATTTT TTCTGTCTAT AGGGAAGCAA
7851 ATTAGATCAT GCATGTGCCT CACCCACCTC TGTTCATG ATTT**CAGGCA**

FIG. 10F

9201 ACTGGACTGC TTGCCCCAGG GCCCGGATGG AAAGCTGGTG TGTCAAGACC
9251 CCTGCAATAC ATATGAGACC CTGACTGAGT ACTGGCGCAG CACAGAGTAT
9301 GGTGTGGGCT ACTCCTGTGA CGCGGGTCTG CACGGCTGGT ACCGG
POLYCLONING SITE OF pBS

FIG. 10H

009230 2405050

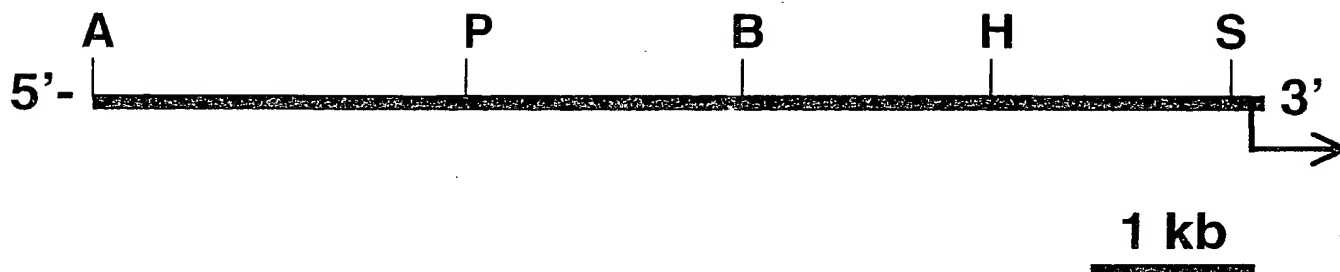


FIG. 11

1 TACTGGCGCA GCACAGAGTA CGGCTCCGGC TACGTCTGTG ATGTCAGTCT
 51 GGGCGGCTGG TACCGCTTCG TGGGCCAGGG CGGCGTGCGC CTGCCCCGAGA
 101 CCTGCGTGCC CGTCCTGCAC TGCAACACGG CCGCGCCTAT GTGGCTCAAC
 151 GGCACGCACC CATCGAGCGA CGAGGGCATC GTGAACCGCG TGGCCTGTGC
 201 GCACTGGAGC GGCGACTGCT GCCTGTGGGA CGCGCCTGTC CAAGTGAAGG
 251 CCTGTGCCGG CGGCTACTAC GTGTACAACC TGACAGAGCC CCCTGAG
 AS14
 AS15
 AS17

FIG. 12

1 ACTATAGGGC ACGCGTGGTC GACGGCCCGG GCTGGTAAAT CTAAAAAA
 51 AAAAAAACA AAAAGAACAT CACTAAGCCC CCCTGCCCTG GCACTTTATT
 101 GGAAGGTCAA GAACACACTC AACCACACAA GAGATGTGAA CATACCTGTG
 151 TGGTACCCAA AGACATCCCC TTTCACACAT ACATGACCCT TCCATTGGGT
 201 TGCACATTGC TGT TAGCTTT TTGTTGGAGA AGGGAGCTAG ACACCTCTAC
 251 ACAACCCCA ACTGGAGTTC TCTGGAACAG AGTAAATACC ATCGTGT CAT
 301 CATGGAGCGC ACACACACTG TGGTCCTGCA ACCTCGATTT GTGTCCTGGC
 351 TCTGCTGCTT ACCAATGAAG CAAGTAGCTT AAACCTTCTG AATCTCAAGT
 401 TTCCTCACCC TCAAACATA GCTAAATACA AAAGTCATTT CCCAGGGCCA
 451 CTGGAGAGGA TTCTATCAGA TAATGGATAG AAGATGCCTA TCCCAGTGT
 501 TGACATATCC TAAGTGCTTA ATACACGAGA GCTCACCATC TTTACTGGTA
 551 TTATTGCACA GAGAAACACA CAAAGTGTC GTGCCCCTGC TAGGTAGAGA
 601 GGGANGCANG GNAAGGAGAT CTGAGCAAAA GGCATAGAAT ATATCAAGCT
 651 GGG

FIG.13A

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CGGGGGAAGG TTTATTTTGT TTCTTTTCAA AGGGGGTCTT GNTCTGTCTC
1
51 AAAGACCNTA AGGACCATGA AAAAATCTCT TTGTNAAAAG TGCCAAGCGG
101 TCCCCACTCT GAATCTGGGC TTTTCTGCCT GCAGAAAGCT GCTCTGAATG
151 TCACGCCAAT GCCACTTGTA CGGTGGACGG GGCTTGCCAC GACCTGCGCC
201 TGCCAGGAGG GCTTCACTGC GACGGCCTCG AATGTGCGGA TCTGGATGAA
251 TGCGCCATTC TGGGGGCGCA CAACTGCTCC GCCACCAACA GCTGCGTGAA
301 CGCGCTGGGC TCCTACACAT GCGTCTGCCC TGAAGGTTTC CTCCTGAGCT
351 CGGAGCTCGG CTGCGAGGAT GTGGACGAGT GTGCAGAGCC AGGGCTCAGC
401 CGCTGCCACG CCCTGGCCAC CTGCATCAAT GGCGAGGGCA ACTACTCATG
451 CGTGTGTCCC GCGGGCTACG TGGGGGACGG GAGGCACTGT GAGTGTTCCC
501 CGGGCTCCTG CGGGCCTGGG CTAGACTGCG TGCGGGAGGG TGACGCGCTA
551 GTGTGCGCTG ACCCGTGCCA GGCGCACCAC ATCCTGGACG AATACTGGCG
601 CAGCACAGAG TACGGCTCCG GCTACGTCTG TGATGTCAGT CTGGGCGGCT
651 GGTAC

FIG. 13B

1 ACTATAGGGC ACGCGTGGTC GACGGCCCCG GCTGGTAAAG ACACCCAGAC
51 TTAGGTTTTG ACAGAGCCTC ATGTTACCA ACCAGAAATG ACATTCACCA
101 CCTAGGATTG AGAAAAAGAA TATTAGGAAC TTTTATTTTC TTCTGAAGTT
151 ATAGCAAAGA AAGGGGAAAA AAAAAACAT TCTTATGGGG GATAAACGGG
201 CAAAGGATAC AAACAGTTCA GAAAAGAATA AATAGTAAGC AAATGAAAAG
251 ATAACCTCCT TTTTCATCAA AGAACCGCAA AAGTAAATAA TGATAAGATG
301 TTTCTCACTT TTCCACAAAG ATGAAAGTTA ATGCCCAGGG TGGCTGAGTA
351 CTGTGCTGGG ATTGTGAACT AACTGTTATA GATCTCTCTG GGGTGCTGTT
401 TGGGAAGAAA CATCGCTGAA AACTGAGCTA CCTCTTTTCC TATGAAATTC
451 CCCTGAGGAG GTGAGTGAGC CGCTGCTGAT CGTCACCCGA GCACTAGGCC
501 AGACAGAAAG AGAAAGCCCT CAAAGAGGCA ATGCTGTGGA TCACTGTCAT
551 ATTCCTGCT CAGCCTGAGT TCACATGTGC CTGATTTTTC TCAATATGGC
601 ATTGCCATTA ACGTGGAATT AGGTCAGGAG ACCTAAGGCT GAACCAAGCC
651 CTGTCATTCT CTGCCCCATG ACTGCGCATC ACCAAAACAG CATCGGCAGT
701 GACTTCCACA GATGGTACCA TTGCTATATG CCTTAACTTG CATCATCTCC
751 TTTAATGGCC ATAACAATTC TAGGACACGG GTATTCTTGT TTTACAGATG
801 ATGAAAATTA CCTCTGGAAG GAAAATTACT GGCACACAAA AAACGCTGAC
851 CAGGATTCAG ATAGACTGAC TCCAAAGTCA GTCTGTTCAT CTACAAAATT
901 ATCTACTTCT CAAGGACCTT CCTTCATGGG AATTCAAATT TCTTGATTCA
951 CAGAGCATCT GGTCCAATGA TGTCTGAATT ATCTGCTGTC TCTGACCTTC

FIG. 14A

1001 AGCCATTCTC AGCTCCTTTC CTGATCACAT TGGGACCCCA GGGGAGCTGG
 1051 CTGAATCTGT GAGGATGGCA TTTGCTTTGG AATTAAGTGG CCACAAGTAC
 1101 ACATCCTGGT GGGGACGATG AGCACCCCTT TTCTCCTGGA GCAGCCTGGC
 1151 TTCAGATTCT GGCCTCTGCT TGGCTCCACT TTGTGCTTTT CAATGACCAA
 1201 GAAAATCCCA GGCCCTTGGA ATTGTTTACT CAGTTAATTT CTA ACTAAAG
 1251 AACCTCTTGT TGCCAAAAGG TATAAAACAG AGCCCTTGTA GCTGTGGGCA
 1301 CAGCTGTGAC CCCCATGTCA ATCATTGTTGG GTCTCTACCT ATTAGGGAAA
 1351 AGAACAACAA CCACCTCACA GCCTAGAAAA GGAAAACACT GTGTCAAAAG
 1401 GGAAAATAT TCCACCCCCA TTAAAATAAT TAAGAAACAG AACCAGAGGA
 1451 TCATTGGAGG AGAGATTGCC AGTGGGGGAC AGATGTATAT ATATAGATAT
 1501 GAAAGTCACC TACTTGTAAG AGGATTAATT CTACCTTTCT GGTTTCAGGT
 1551 AAGGCTATCT GCAGCTCTCA CTTCTCCTAG CCACTTCTCC CATCTAGTCT
 1601 TTGCTGGCTC CCATTCTGTT TGAAGGATGG

FIG.14B

```
$ type guromodulinpromoter18full.pair;1
BESTFIT of: Guromodulinpromoter18full  check: 3852  from: 1  to: 1630
```

```
to: mouseThppromoterfull.  check: 5595  from: 1  to: 9343
```

```
Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgapdna.Cmp
CompCheck: 2335
```

```
Gap Weight:      50      Average Match: 10.000
Length Weight:   3      Average Mismatch: -9.000

Quality: 1617      Length: 534
Ratio: 3.177      Gaps: 15
Percent Similarity: 74.385  Percent Identity: 74.385
```

```
Match display thresholds for the alignment(s):
| = IDENTITY
: = 5
. = 1
```

```
Guromodulinpromoter18full x Thppromoterfull. March 24, 2000 16:31 ..
```

```
1121 AGCACCCCTTTTCTCCTGGAGCAGCCTGGCTTCAGA.....T 1157
    | | | | | | | | | | | | | | | | | | | | | |
6677 AACATTTCCTTTTATCCTAACACAGTCTGACTTCAGATATACTGTCTTTTT 6726

1158 TCTGGCCTCT...GCTTGGCTCCACTTTGTGCTTTTCAATGACCAAGAAA 1204
    | | | | | | | | | | | | | | | | | | | | | |
6727 CCTGGCTCCTTGGGCTTAGGTCTACCTTGTCTTGGCCAGGTCCAAGAAA 6776

1205 A.TCCCAGGCCCTTGGAATTGTTTACTCAGTTAATTTCTAACTAAAGAAC 1253
    | | | | | | | | | | | | | | | | | | | | | |
6777 AGGCCCAGAACCTTGGCACTGTTTTGCCAGTTAATGTCTAACTGAGGAAT 6826

1254 CTCTTGTTGCCAAAAGGTATAAAACAGAGCCCTTGTAGCTGTGGGCACAG 1303
    | | | | | | | | | | | | | | | | | | | | | |
6827 GTCTTGCTGCCAAAAGGT.GAAAACAGAGACCTTGTATTTCCAGGCACAG 6875

1304 CTGTGACCCCATGTCAATCATTTGGGGTCTCTACCTATTAGGG...AAA 1350
    | | | | | | | | | | | | | | | | | | | | | |
6876 GTGTGACCCCAATGTCAATCATTT..TGTGTCTAACTCCCAGGGGAAAAA 6923

1351 AGAACAACAACCACCTCACAGCCTAGAAAAGGAAAACACTGTGTCAAAAAG 1400
    | | | | | | | | | | | | | | | | | | | | | |
6924 CTAACAACAACAGACTCATGGCTTGGAAGGTGAATTCTATGCCAAAAG 6973

1401 GGAA.AAATATTCCACCCCATTAATAAAT.TAAGA.AACAGAACCAGA 1447
    | | | | | | | | | | | | | | | | | | | | | |
6974 GGAAGGAAAGTTCTACCCCAAGAAACAATCTCAGAGGGCAGAAAGCAGA 7023

1448 GGATCATTGGAGGAGAGATTGCCAGTGGGGGACAGATGTATATATATAGA 1497
    | | | | | | | | | | | | | | | | | | | | | |
7024 GAATAATCTGAGG.GAGAGGGCCAGCCAAGGGCAG..GCAAGTATATATT 7070

1498 TATGAAAGTCACCTACTTGTAAAAGGATTAATTCTACCTTTCTGGTTTCA 1547
    | | | | | | | | | | | | | | | | | | | | | |
7071 GATCACAGGCACTTACTTGTGAATGGACCAGTCCT...GTCCTGGGTTC 7117
```

FIG.15A

[illegible]

FIG. 15B

000000" 24050950

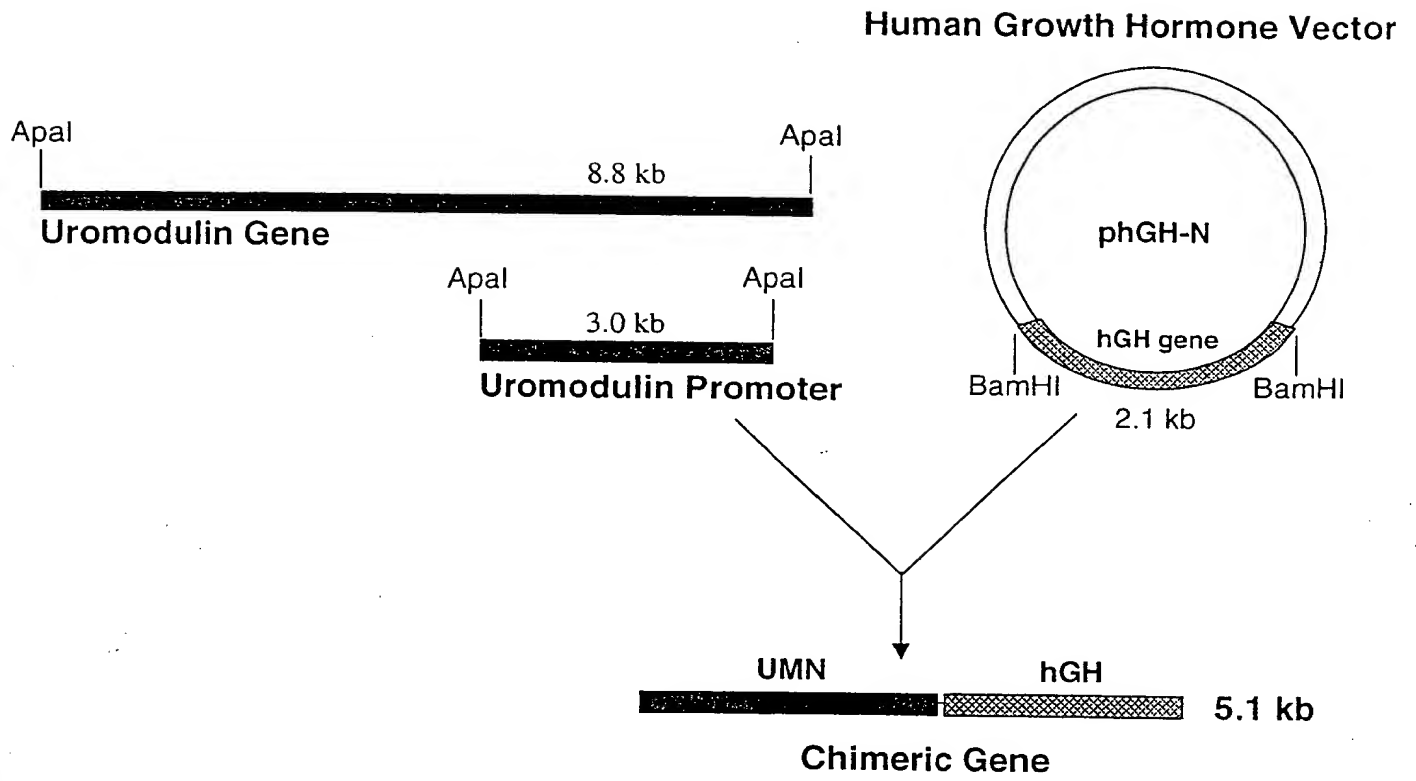


FIG.16

000000 24050950

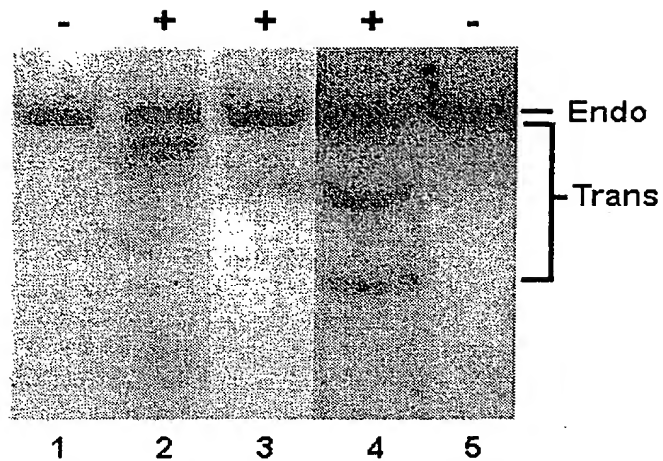


FIG. 17

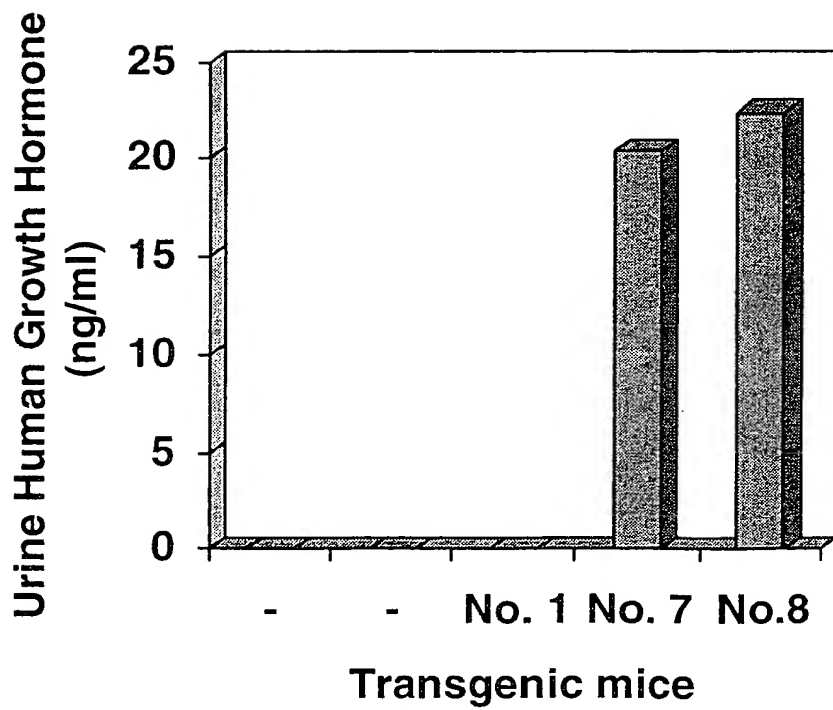


FIG. 18

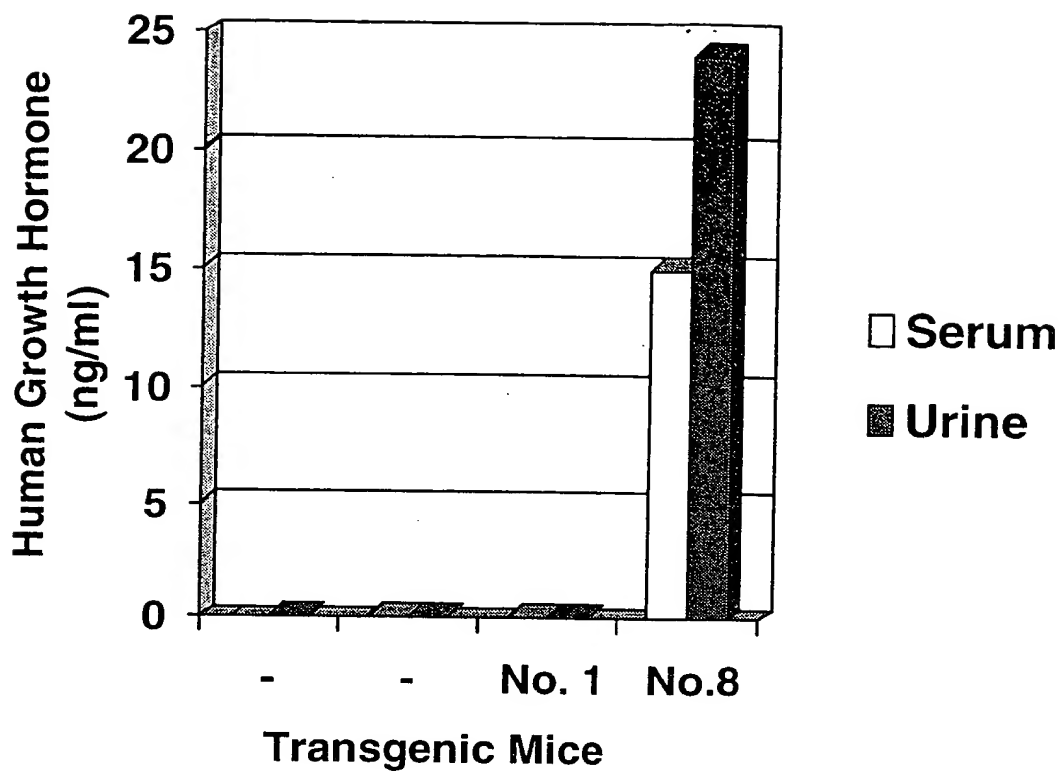


FIG. 19

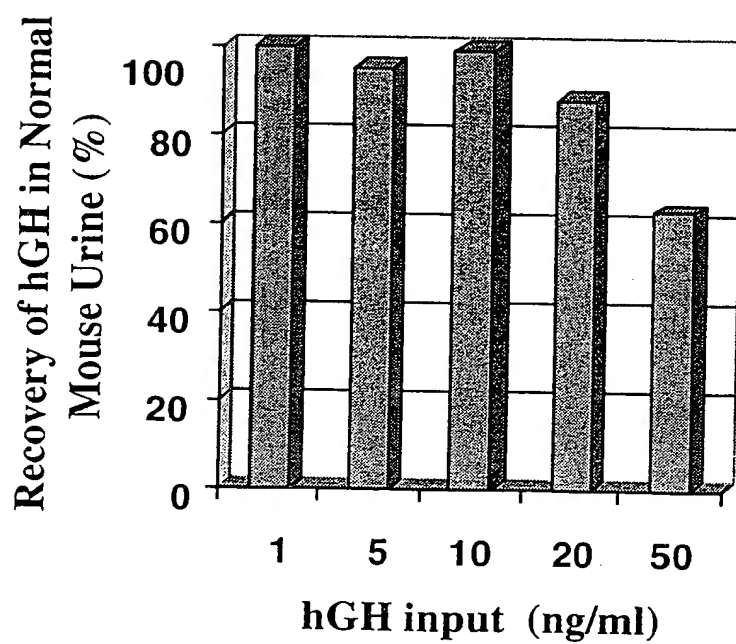


FIG. 20